

SEQUENCE LISTING

<110> Prof. Dr. Axel R. Zander

<120> Use of CD34 or a Polypeptide derived therefrom as
Cell Surface/Gene Transfer Marker

<130> 35-204

<140>

<141>

<160> 10

<170> PatentIn Ver. 2.0

<210> 1

<211> 1122

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1122)

<223> CD34 (complete length)

<400> 1

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ggg	ttc	atg	agt	ctt	gac	aac	aac	ggt	act	gct	acc	cca	gag	tta	cct	96
Gly	Phe	Met	Ser	Leu	Asp	Asn	Asn	Gly	Thr	Ala	Thr	Pro	Glu	Leu	Pro	
			20					25					30			

acc	cag	gga	aca	ttt	tca	aat	gtt	tct	aca	aat	gta	tcc	tac	caa	gaa	144
Thr	Gln	Gly	Thr	Phe	Ser	Asn	Val	Ser	Thr	Asn	Val	Ser	Tyr	Gln	Glu	
		35					40				45					

act	aca	aca	cct	agt	acc	ctt	gga	agt	acc	agc	ctg	cac	cct	gtg	tct	192
Thr	Thr	Thr	Pro	Ser	Thr	Leu	Gly	Ser	Thr	Ser	Leu	His	Pro	Val	Ser	
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caa	cat	ggc	aat	gag	gcc	aca	aca	aac	atc	aca	gaa	acg	aca	gtc	aaa	240
Gln	His	Gly	Asn	Glu	Ala	Thr	Thr	Asn	Ile	Thr	Glu	Thr	Thr	Val	Lys	
65				70				75						80		

ttc	aca	tct	acc	tct	gtg	ata	acc	tca	gtt	tat	gga	aac	aca	aac	tct	288
Phe	Thr	Ser	Thr	Ser	Val	Ile	Thr	Ser	Val	Tyr	Gly	Asn	Thr	Asn	Ser	
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tct	gtc	cag	tca	cag	acc	tct	gta	atc	agc	aca	gtg	ttc	acc	acc	cca	336
Ser	Val	Gln	Ser	Gln	Thr	Ser	Val	Ile	Ser	Thr	Val	Phe	Thr	Thr	Pro	

			100				105				110							
gcc	aac	gtt	tca	act	cca	gag	aca	acc	ttg	aag	cct	agc	ctg	tca	cct	384		
Ala	Asn	Val	Ser	Thr	Pro	Glu	Thr	Thr	Leu	Lys	Pro	Ser	Leu	Ser	Pro			
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gga	aat	gtt	tca	gac	ctt	tca	acc	act	agc	act	agc	ctt	gca	aca	tct	432		
Gly	Asn	Val	Ser	Asp	Leu	Ser	Thr	Thr	Ser	Thr	Ser	Leu	Ala	Thr	Ser			
			130				135				140							
ccc	act	aaa	ccc	tat	aca	tca	tct	tct	cct	atc	cta	agt	gac	atc	aag	480		
Pro	Thr	Lys	Pro	Tyr	Thr	Ser	Ser	Ser	Pro	Ile	Leu	Ser	Asp	Ile	Lys			
145			150				155				160							
gca	gaa	atc	aaa	tgt	tca	ggc	atc	aga	gaa	gtg	aaa	ttg	act	cag	ggc	528		
Ala	Glu	Ile	Lys	Cys	Ser	Gly	Ile	Arg	Glu	Val	Lys	Leu	Thr	Gln	Gly			
			165				170				175							
atc	tgc	ctg	gag	caa	aat	aag	acc	tcc	agc	tgt	gcg	gag	ttt	aag	aag	576		
Ile	Cys	Leu	Glu	Gln	Asn	Lys	Thr	Ser	Ser	Cys	Ala	Glu	Phe	Lys	Lys			
			180				185				190							
gac	agg	gga	gag	ggc	ctg	gcc	cga	gtg	ctg	tgt	ggg	gag	gag	cag	gct	624		
Asp	Arg	Gly	Glu	Gly	Leu	Ala	Arg	Val	Leu	Cys	Gly	Glu	Glu	Gln	Ala			
			195				200				205							
gat	gct	gat	gct	ggg	gcc	cag	gta	tgc	tcc	ctg	ctc	ctt	gcc	cag	tct	672		
Asp	Ala	Asp	Ala	Gly	Ala	Gln	Val	Cys	Ser	Leu	Leu	Leu	Ala	Gln	Ser			
			210				215				220							
gag	gtg	agg	cct	cag	tgt	cta	ctg	ctg	gtc	ttg	gcc	aac	aga	aca	gaa	720		
Glu	Val	Arg	Pro	Gln	Cys	Leu	Leu	Leu	Val	Leu	Ala	Asn	Arg	Thr	Glu			
225			230				235				240							
att	tcc	agc	aaa	ctc	caa	ctt	atg	aaa	aag	cac	caa	tct	gac	ctg	aaa	768		
Ile	Ser	Ser	Lys	Leu	Gln	Leu	Met	Lys	Lys	His	Gln	Ser	Asp	Leu	Lys			
			245				250				255							
aag	ctg	ggg	atc	cta	gat	ttc	act	gag	caa	gat	gtt	gca	agc	cac	cag	816		
Lys	Leu	Gly	Ile	Leu	Asp	Phe	Thr	Glu	Gln	Asp	Val	Ala	Ser	His	Gln			
			260				265				270							
agc	tat	tcc	caa	aag	acc	ctg	att	gca	ctg	gtc	acc	tcg	gga	gcc	ctg	864		
Ser	Tyr	Ser	Gln	Lys	Thr	Leu	Ile	Ala	Leu	Val	Thr	Ser	Gly	Ala	Leu			
			275				280				285							
ctg	gct	gtc	ttg	ggc	atc	act	ggc	tat	ttc	ctg	atg	aat	cgc	cgc	agc	912		
Leu	Ala	Val	Leu	Gly	Ile	Thr	Gly	Tyr	Phe	Leu	Met	Asn	Arg	Arg	Ser			
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tgg	agc	ccc	aca	gga	gaa	agg	ctg	ggc	gaa	gac	cct	tat	tac	acg	gaa	960		
Trp	Ser	Pro	Thr	Gly	Glu	Arg	Leu	Gly	Glu	Asp	Pro	Tyr	Tyr	Thr	Glu			
305			310				315				320							
aac	ggt	gga	ggc	cag	ggc	tat	agc	tca	gga	cct	ggg	acc	tcc	cct	gag	1008		
Asn	Gly	Gly	Gly	Gln	Gly	Tyr	Ser	Ser	Gly	Pro	Gly	Thr	Ser	Pro	Glu			
			325				330				335							

Leu	Ala	Val	Leu	Gly	Ile	Thr	Gly	Tyr	Phe	Leu	Met	Asn	Arg	Arg	Ser
290						295					300				
Trp	Ser	Pro	Thr	Gly	Glu	Arg	Leu	Gly	Glu	Asp	Pro	Tyr	Tyr	Thr	Glu
305					310					315					320
Asn	Gly	Gly	Gly	Gln	Gly	Tyr	Ser	Ser	Gly	Pro	Gly	Thr	Ser	Pro	Glu
				325					330					335	
Ala	Gln	Gly	Lys	Ala	Ser	Val	Asn	Arg	Gly	Ala	Gln	Glu	Asn	Gly	Thr
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Gly	Gln	Ala	Thr	Ser	Arg	Asn	Gly	His	Ser	Ala	Arg	Gln	His	Val	Val
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Ala	Asp	Thr	Glu	Leu											
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<210> 3
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 <213> Homo sapiens

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 <222> (1)..(951)
 <223> CD34 (truncated variant)

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1				5				10						15		
ggg	ttc	atg	agt	ctt	gac	aac	aac	ggg	act	gct	acc	cca	gag	tta	cct	96
Gly	Phe	Met	Ser	Leu	Asp	Asn	Asn	Gly	Thr	Ala	Thr	Pro	Glu	Leu	Pro	
			20					25					30			
acc	cag	gga	aca	ttt	tca	aat	gtt	tct	aca	aat	gta	tcc	tac	caa	gaa	144
Thr	Gln	Gly	Thr	Phe	Ser	Asn	Val	Ser	Thr	Asn	Val	Ser	Tyr	Gln	Glu	
			35				40					45				
act	aca	aca	cct	agt	acc	ctt	gga	agt	acc	agc	ctg	cac	cct	gtg	tct	192
Thr	Thr	Thr	Pro	Ser	Thr	Leu	Gly	Ser	Thr	Ser	Leu	His	Pro	Val	Ser	
			50			55					60					
caa	cat	ggc	aat	gag	gcc	aca	aca	aac	atc	aca	gaa	acg	aca	gtc	aaa	240
Gln	His	Gly	Asn	Glu	Ala	Thr	Thr	Asn	Ile	Thr	Glu	Thr	Thr	Val	Lys	
65					70				75						80	
ttc	aca	tct	acc	tct	gtg	ata	acc	tca	gtt	tat	gga	aac	aca	aac	tct	288
Phe	Thr	Ser	Thr	Ser	Val	Ile	Thr	Ser	Val	Tyr	Gly	Asn	Thr	Asn	Ser	
				85				90						95		
tct	gtc	cag	tca	cag	acc	tct	gta	atc	agc	aca	gtg	ttc	acc	acc	cca	336
Ser	Val	Gln	Ser	Gln	Thr	Ser	Val	Ile	Ser	Thr	Val	Phe	Thr	Thr	Pro	
			100					105					110			

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Ala Asn Val Ser Thr Pro Glu Thr Thr Leu Lys Pro Ser Leu Ser Pro	
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gga aat gtt tca gac ctt tca acc act agc act agc ctt gca aca tct	432
Gly Asn Val Ser Asp Leu Ser Thr Thr Ser Thr Ser Leu Ala Thr Ser	
130 135 140	
ccc act aaa ccc tat aca tca tct tct cct atc cta agt gac atc aag	480
Pro Thr Lys Pro Tyr Thr Ser Ser Ser Pro Ile Leu Ser Asp Ile Lys	
145 150 155 160	
gca gaa atc aaa tgt tca ggc atc aga gaa gtg aaa ttg act cag ggc	528
Ala Glu Ile Lys Cys Ser Gly Ile Arg Glu Val Lys Leu Thr Gln Gly	
165 170 175	
atc tgc ctg gag caa aat aag acc tcc agc tgt gcg gag ttt aag aag	576
Ile Cys Leu Glu Gln Asn Lys Thr Ser Ser Cys Ala Glu Phe Lys Lys	
180 185 190	
gac agg gga gag ggc ctg gcc cga gtg ctg tgt ggg gag gag cag gct	624
Asp Arg Gly Glu Gly Leu Ala Arg Val Leu Cys Gly Glu Glu Gln Ala	
195 200 205	
gat gct gat gct ggg gcc cag gta tgc tcc ctg ctc ctt gcc cag tct	672
Asp Ala Asp Ala Gly Ala Gln Val Cys Ser Leu Leu Leu Ala Gln Ser	
210 215 220	
gag gtg agg cct cag tgt cta ctg ctg gtc ttg gcc aac aga aca gaa	720
Glu Val Arg Pro Gln Cys Leu Leu Leu Val Leu Ala Asn Arg Thr Glu	
225 230 235 240	
att tcc agc aaa ctc caa ctt atg aaa aag cac caa tct gac ctg aaa	768
Ile Ser Ser Lys Leu Gln Leu Met Lys Lys His Gln Ser Asp Leu Lys	
245 250 255	
aag ctg ggg atc cta gat ttc act gag caa gat gtt gca agc cac cag	816
Lys Leu Gly Ile Leu Asp Phe Thr Glu Gln Asp Val Ala Ser His Gln	
260 265 270	
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Ser Tyr Ser Gln Lys Thr Leu Ile Ala Leu Val Thr Ser Gly Ala Leu	
275 280 285	
ctg gct gtc ttg ggc atc act ggc tat ttc ctg atg aat cgc cgc agc	912
Leu Ala Val Leu Gly Ile Thr Gly Tyr Phe Leu Met Asn Arg Arg Ser	
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<211> 316
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 <213> Homo sapiens

<400> 4

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Thr	Thr	Thr	Pro	Ser	Thr	Leu	Gly	Ser	Thr	Ser	Leu	His	Pro	Val	Ser
	50					55					60				
Gln	His	Gly	Asn	Glu	Ala	Thr	Thr	Asn	Ile	Thr	Glu	Thr	Thr	Val	Lys
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Phe	Thr	Ser	Thr	Ser	Val	Ile	Thr	Ser	Val	Tyr	Gly	Asn	Thr	Asn	Ser
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Ser	Val	Gln	Ser	Gln	Thr	Ser	Val	Ile	Ser	Thr	Val	Phe	Thr	Thr	Pro
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Ala	Asn	Val	Ser	Thr	Pro	Glu	Thr	Thr	Leu	Lys	Pro	Ser	Leu	Ser	Pro
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Gly	Asn	Val	Ser	Asp	Leu	Ser	Thr	Thr	Ser	Thr	Ser	Leu	Ala	Thr	Ser
	130					135					140				
Pro	Thr	Lys	Pro	Tyr	Thr	Ser	Ser	Ser	Pro	Ile	Leu	Ser	Asp	Ile	Lys
145					150					155					160
Ala	Glu	Ile	Lys	Cys	Ser	Gly	Ile	Arg	Glu	Val	Lys	Leu	Thr	Gln	Gly
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Ile	Cys	Leu	Glu	Gln	Asn	Lys	Thr	Ser	Ser	Cys	Ala	Glu	Phe	Lys	Lys
			180					185					190		
Asp	Arg	Gly	Glu	Gly	Leu	Ala	Arg	Val	Leu	Cys	Gly	Glu	Glu	Gln	Ala
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Asp	Ala	Asp	Ala	Gly	Ala	Gln	Val	Cys	Ser	Leu	Leu	Leu	Ala	Gln	Ser
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Glu	Val	Arg	Pro	Gln	Cys	Leu	Leu	Leu	Val	Leu	Ala	Asn	Arg	Thr	Glu
225					230					235					240
Ile	Ser	Ser	Lys	Leu	Gln	Leu	Met	Lys	Lys	His	Gln	Ser	Asp	Leu	Lys
			245						250					255	
Lys	Leu	Gly	Ile	Leu	Asp	Phe	Thr	Glu	Gln	Asp	Val	Ala	Ser	His	Gln
			260					265					270		
Ser	Tyr	Ser	Gln	Lys	Thr	Leu	Ile	Ala	Leu	Val	Thr	Ser	Gly	Ala	Leu
		275					280					285			
Leu	Ala	Val	Leu	Gly	Ile	Thr	Gly	Tyr	Phe	Leu	Met	Asn	Arg	Arg	Ser
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Trp	Ser	Pro	Thr	Gly	Glu	Arg	Leu	Glu	Leu	Glu	Pro				
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 <213> Homo sapiens

<220>
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gag gtg agg cct cag tgt cta ctg ctg gtc ttg gcc aac aga aca gaa	720
Glu Val Arg Pro Gln Cys Leu Leu Leu Val Leu Ala Asn Arg Thr Glu	
225 230 235 240	
att tcc agc aaa ctc caa ctt atg aaa aag cac caa tct gac ctg aaa	768
Ile Ser Ser Lys Leu Gln Leu Met Lys Lys His Gln Ser Asp Leu Lys	
245 250 255	
aag ctg ggg atc cta gat ttc act gag caa gat gtt gca agc cac cag	816
Lys Leu Gly Ile Leu Asp Phe Thr Glu Gln Asp Val Ala Ser His Gln	
260 265 270	
agc tat tcc caa aag acc ctg att gca ctg gtc acc tcg gga gcc ctg	864
Ser Tyr Ser Gln Lys Thr Leu Ile Ala Leu Val Thr Ser Gly Ala Leu	
275 280 285	
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Leu Ala Val Leu Gly Ile Thr Gly Tyr Phe Leu Met Asn	
290 295 300	

<210> 6
 <211> 301
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Thr Thr Thr Pro Ser Thr Leu Gly Ser Thr Ser Leu His Pro Val Ser
 50 55 60
 Gln His Gly Asn Glu Ala Thr Thr Asn Ile Thr Glu Thr Thr Val Lys
 65 70 75 80

 Phe Thr Ser Thr Ser Val Ile Thr Ser Val Tyr Gly Asn Thr Asn Ser
 85 90 95
 Ser Val Gln Ser Gln Thr Ser Val Ile Ser Thr Val Phe Thr Thr Pro
 100 105 110
 Ala Asn Val Ser Thr Pro Glu Thr Thr Leu Lys Pro Ser Leu Ser Pro
 115 120 125
 Gly Asn Val Ser Asp Leu Ser Thr Thr Ser Thr Ser Leu Ala Thr Ser
 130 135 140
 Pro Thr Lys Pro Tyr Thr Ser Ser Ser Pro Ile Leu Ser Asp Ile Lys
 145 150 155 160
 Ala Glu Ile Lys Cys Ser Gly Ile Arg Glu Val Lys Leu Thr Gln Gly
 165 170 175

Ile Cys Leu Glu Gln Asn Lys Thr Ser Ser Cys Ala Glu Phe Lys Lys
 180 185 190
 Asp Arg Gly Glu Gly Leu Ala Arg Val Leu Cys Gly Glu Glu Gln Ala
 195 200 205
 Asp Ala Asp Ala Gly Ala Gln Val Cys Ser Leu Leu Leu Ala Gln Ser
 210 215 220
 Glu Val Arg Pro Gln Cys Leu Leu Leu Val Leu Ala Asn Arg Thr Glu
 225 230 235 240
 Ile Ser Ser Lys Leu Gln Leu Met Lys Lys His Gln Ser Asp Leu Lys
 245 250 255
 Lys Leu Gly Ile Leu Asp Phe Thr Glu Gln Asp Val Ala Ser His Gln
 260 265 270
 Ser Tyr Ser Gln Lys Thr Leu Ile Ala Leu Val Thr Ser Gly Ala Leu
 275 280 285
 Leu Ala Val Leu Gly Ile Thr Gly Tyr Phe Leu Met Asn
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 <213> Artificial sequence

<220>
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 <213> Artificial sequence

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<210> 9
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 <212> DNA
 <213> Artificial sequence

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47

